

Figure 1

Gene and AA sequence

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      M L G K F S Q T C Y N S A I Q G S V L T S T C E R T N G G
1 AGGAGGACAG CTATGCTGGG CAAGTTCAGC CAGACCTGCT ACACAGCGC GATTCAGGCG AGCGTTCTGA CCAGCACCTG CGAACGTACC AATGGTGGCT
  TCCTCCTGTC GATACGACCC GTTCAAGTCG GTCTGACGA TGTGTGCGG CTAAGTCCG TCGCAAGACT GGTGCGGAC GCTTGCATGG TTACCACCGA

      Y N T S S I D L N S V I E N V D G S L K W Q P S N F I E T C R N T Q
101 ACAACACTTC TAGCATTGAT CTGAACAGCG TGATTGAGAA TGTGGATGGC TCTCTGAAT GGCAGCCGAG CAACTTCATT GAAACCTGTC GCAACACCCA
  TGTGTGAAG ATCGTAACTA GACTTGTCCG ACTAATCTTT ACACCTACCG AGAGACTTAA CCGTCGGCTC GTTGAAGTAA CTTTGGACAG CGTTGTGGGT

      L A G S S E L A A E C K T R A Q O F V S T K I N L D D H I A N I D
201 GCTGGCGGCG AGCTCTGAAC TGGCGGCAGA ATGCAAGACT CGCGCGCAGC AGTTTGTGAG CACCAAGATC AACCTGGACG ATCACATCGC GAACATTGAT
  CGACCGCCCG TCGAGACTTG ACCGCCGTCT TACGTTCTGA GCGCGCGTCG TCAAAACTC GTGGTCTAG TTGGACCTGC TAGTGTAGCG CTTGTAACTA

      G T L K Y E #
301 GGCACCCCTGA AGTATGAATA A
  CCGTGGGACT TCATACTTAT T

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Figure 2

AA alignment

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      .....LGKFSQTCYN SAIQGSVLTSTCERTNGGYNTSSIDLNSVIENVDSGLKWQPSNFI 55
      |||||
      MLGKFSQTCYN SAIQGSVLTSTCERTNGGYNTSSIDLNSVIENVDSGLKWQPSNFI 56

      ETCRNTQLAGSSELAAECKTRAQQFVSTKINLDDHIANIDGTLKYE* 101
      |||||
      ETCRNTQLAGSSELAAECKTRAQQFVSTKINLDDHIANIDGTLKYE* 102

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Figure 3

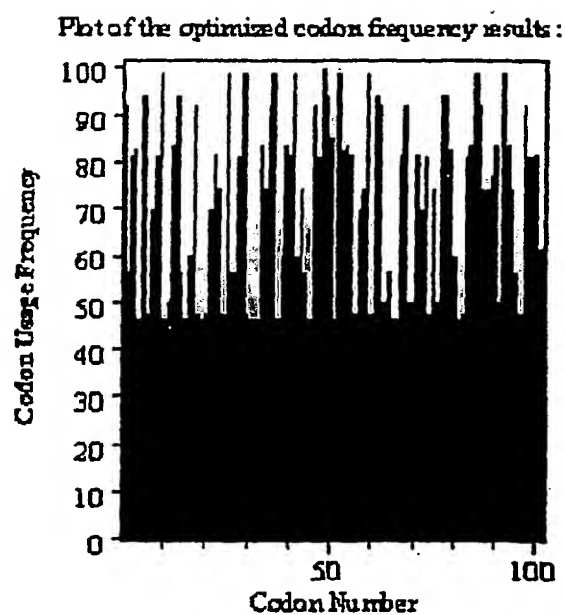


Figure 4

1 atccggatat agttccctct ttacgcaaaa aacccctcaa gaccctgita gaggccccaa
 61 ggggttatgc tagtatgc tcagcgggtg cagcagccaa ctacgttcc ttccgggtt
 121 tgitagcagc cggatcicag tgggtgggtt ggtgggtc gacatcccg gggcttccg
 181 gggcgagttc tggctggcta gcccgttga tctcaggtt ttacatctc aggttgcct
 241 caatgtcgc gatgtatcg tccaggttga tcttgggtc cacaactgc tgcgcggag
 301 tctgcaatc tgcgcgcag tccaggtcgc cgcgcagctg ggtgttgcga caggttcaa
 361 tgaagtgtc cggctgcat ttacagagagc catccacat ctcacacag ctgttcagat
 421 caatgtcaga aggtgttag ccacatggg tccgttcga ggtgtgtgc agaacgtgc
 481 cctgaatcgc gctgtgtg caggtctggc tgaactgcc caggtatgt atatctctt
 541 cttaaagta aacaaaatta ttctagagg ggaattgta tccgtcaca attccctat
 601 agtgagtcgt attaatctg cgggatcag atctcgtatc tctacgccg acgcatcgtg
 661 gccggcatca ccggcgccac aggtgcggtt gctggcgctt atatcgcca catcaccgat
 721 ggggaagatc gggctcgcca ctccgggtc atgagcgctt gttcggcgt gggtatggtg
 781 gcaggccccc tggccggggg actgttgggc gccatctct tgcagtcacc attccttgcg
 841 gcggcggtgc tcaacggcct caacctacta ctgggtgct tctaatgca ggagtcgat
 901 aaggagagc gtcgagatcc cggacacat cgaatggcg aaaaccttc gcggtatgg
 961 atgtagcgc ccggaagaga gtcaattcag ggtgttgaat gtgaaccag taacgtata
 1021 cgatgtcga gagtatccg gtgtctctta tcagaccgt tcccgcgtg tgaaccaggc
 1081 cagccagtt tctcgaaaa cgcgggaaaa agtggagcg gcgatggcg agctgaatta
 1141 cattccaac cgcgtggcac acaactggc gggcaaacag tctgtctga ttggcgttc
 1201 cactccagt ctggccctgc acgcgccgt ccaaattgc gcggcgatta aatctcgcg
 1261 cgatcaactg ggtgccagcg tgggtgtgc gatgtagaa cgaagcgcg tgaagcctg
 1321 taaagggcg gtgcacaatc ttctcgca acgcgtcagt gggctgatca ttaactatc
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 1621 caatcaaat cagccgatag cggaaaggga aggcgactg agtgccatg ccggtttca
 1681 acaaacatg caaatgtga atgagggcat cgttcccat gcgatgctg ttccaacga
 1741 tcagatggcg ctggcgcaa tgcgcgccat taccagatc gggctgcgc ttggtgcga
 1801 tatctcgga tggggatag acgataccga agacagctc tttatatcc cgcgttaac
 1861 caccatcaa caggatttc gcctgtctgg gcaaaccagc tggaccgct tctgcaact
 1921 ctctcagggc caggcggtga agggcaatca cgtgttccc gctcactg tgaagaagaa
 1981 aaccacctg gcgccaata cgaaccgc ctctcccg cgttggcg attcataat
 2041 gcagctggca cgacaggtt cccgactgga aagcggcg tgaagcgaac gcaattaat
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 2161 cagtgcgtc ctccgggtg gcgcggggca tgactatct cgcgcactt atgactgtc
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 2881 cggaggcatc agtgacaaa caggaaaaa cgccttaa catggccgc ttatcagaa
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Figure 4 (Continued)

3001 tctgtgaatc gcttcacgac cacgctgatg agcttiaccg cagctgccic gcgcgtttcg
 3061 gtgatgacgg tgaataacctc tgacacatgc agctcccga gacgggcaca gcttgtctgt
 3121 aagcggatgc cgggagcaga caagcccgtc agggcgcgtc agcgggtgtt ggccgggtgc
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 4081 cgcagaaaaa aaggatcga agaagatcct ttgatcttt ctacggggc tgacgtcag
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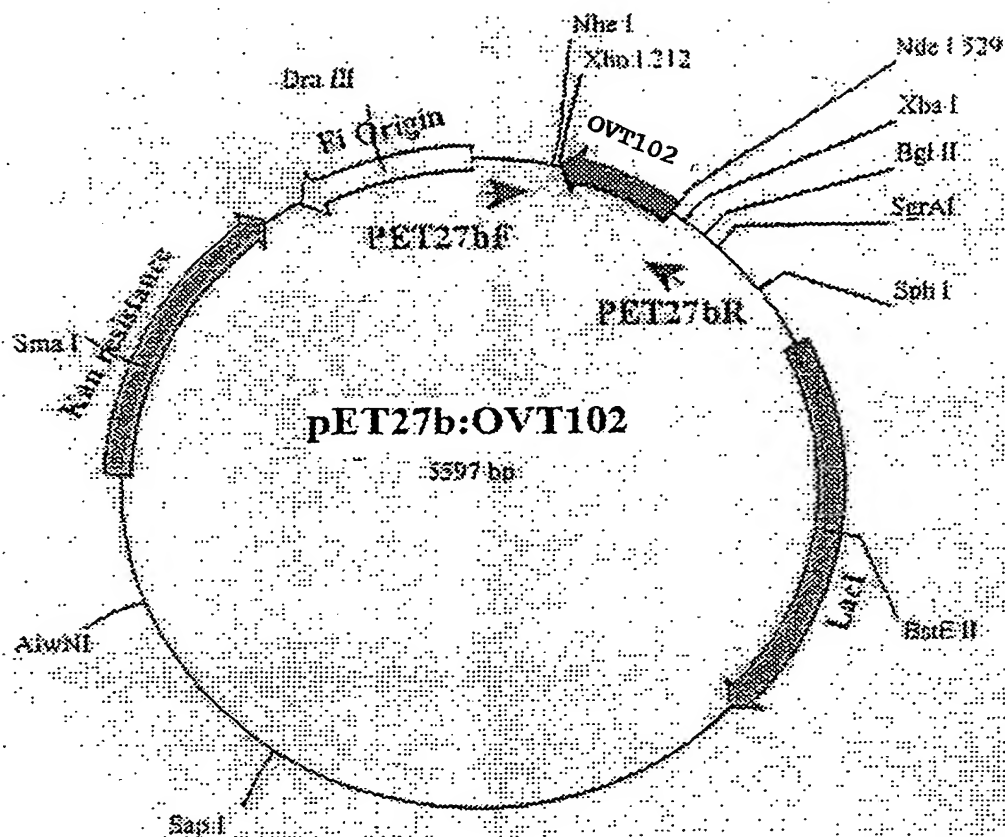
Figure 5

FIGURE 6



1 2 3 4 5 6 7 8 9 10 11 12

FIGURE 7

